

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.

(FILE 'HOME' ENTERED AT 09:14:20 ON 11 JAN 2003)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, CANCERLIT' ENTERED AT 09:14:46 ON
11 JAN 2003

L1 1327 S ((NILSON L?) OR (POTTER H?) OR (ARENDASH G?))/AU
L2 7605 S ANTICHYMOTRYPSIN
L3 90 S L1 AND L2
L4 170602 S TRANSGENIC
L5 10 S L3 AND L4
L6 4 DUP REM L5 (6 DUPLICATES REMOVED)
L7 46 S MUCKE L?/AU AND ABRAHAM C?/AU
L8 10 S L2 AND L7
L9 4 DUP REM L8 (6 DUPLICATES REMOVED)
L10 109110 S TRANSGENIC(S) (MOUSE OR MICE)
L11 48 S L2 AND L10
L12 25 DUP REM L11 (23 DUPLICATES REMOVED)

L Number	Hits	Search Text	DB	Time stamp
1	7049	NILSSON.IN. POTTER.IN. ARENDASH.IN.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:49
2	1053327	antichymotrypsin act	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:49
3	535	antichymotrypsin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:49
4	21	(NILSSON.IN. POTTER.IN. ARENDASH.IN.) and antichymotrypsin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:51
5	24835	transgenic	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:51
6	4	((NILSSON.IN. POTTER.IN. ARENDASH.IN.) and antichymotrypsin) and transgenic	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:55
7	125	antichymotrypsin and transgenic	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:55
8	173627	mouse	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:55
9	9167	transgenic with mouse	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:56
10	105	antichymotrypsin and (transgenic with mouse)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/01/11 08:56

ExPASy Home page	Site Map	Search ExPASy	Contact us	SWISS-PROT
Hosted by NCSC US Mirror sites: Bolivia Canada China Korea Switzerland Taiwan				

NiceProt View of SWISS-PROT: P01011

[Printer-friendly view](#)[Quick BlastP search](#)

[\[General\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

General information about the entry

Entry name **AACT_HUMAN**
 Primary accession number **P01011**
 Secondary accession number **Q13703**
 Entered in SWISS-PROT in **Release 01, July 1986**
 Sequence was last modified in **Release 19, August 1991**
 Annotations were last modified in **Release 41, June 2002**

Name and origin of the protein

Protein name **Alpha-1-antichymotrypsin [Precursor]**
 Synonym **ACT**
 Gene name **SERPINA3 or AACT**
 From **Homo sapiens (Human) [TaxID: 9606]**
 Taxonomy **Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.**

References

- [1] SEQUENCE FROM NUCLEIC ACID.
 MEDLINE=84080367; PubMed=6606438; [NCBI, ExPASy, EBI, Israel, Japan]
 Chandra T., Stackhouse R., Kidd V.J., Robson K.J.H., Woo S.L.C.;
 "Sequence homology between human alpha 1-antichymotrypsin, alpha 1-antitrypsin, and antithrombin III."; *Biochemistry* 22:5055-5061(1983).
- [2] SEQUENCE FROM NUCLEIC ACID, AND VARIANTS BOCHUM-1 AND BONN-1.
 MEDLINE=94063919; PubMed=8244391; [NCBI, ExPASy, EBI, Israel, Japan]
 Poller W., Faber J.-P., Weidinger S., Tief K., Scholz S., Fischer M., Olek K., Kirchgesser M., Heidtmann H.-H.;
 "A leucine-to-proline substitution causes a defective alpha 1-antichymotrypsin allele associated with familial obstructive lung disease."; *Genomics* 17:740-743(1993).
- [3] SEQUENCE FROM NUCLEIC ACID.
 TISSUE=Brain, and Skin;
 Strausberg R.;
 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
- [4] SEQUENCE OF 87-129 FROM NUCLEIC ACID.
 MEDLINE=90110106; PubMed=2404007; [NCBI, ExPASy, EBI, Israel, Japan]
 Rubin H., Wang Z., Nickbarg E.B., McLamev S., Naidoo N., Schoenberger O.L., Johnson J.L., Cooperman B.S.;
 "Cloning, expression, purification, and biological activity of recombinant native and variant human alpha 1-antichymotrypsins."; *J. Biol. Chem.* 265:1199-1207(1990).
- [5] SEQUENCE OF 22-423 FROM NUCLEIC ACID.
 Rubin H.;
 Submitted (OCT-1989) to the EMBL/GenBank/DDBJ databases.
- [6] SEQUENCE OF N-TERMINUS.
 MEDLINE=89323223; PubMed=2787670; [NCBI, ExPASy, EBI, Israel, Japan]
 Lindmark B., Hilja H., Alan R., Eriksson S.;
 "The microheterogeneity of desialylated alpha 1-antichymotrypsin: the occurrence of two amino-terminal isoforms, one lacking a His-Pro dipeptide.";

- Biochim. Biophys. Acta 997:90-95(1989).
- [7] ACTIVE SITE.
MEDLINE=84032476; PubMed=6556193; [NCBI, ExPASy, EBI, Israel, Japan]
Mori M., Travis J.;
"Amino acid sequence at the reactive site of human alpha 1-antichymotrypsin.";
J. Biol. Chem. 258:12749-12752(1983).
- [8] X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE=91202538; PubMed=2016749; [NCBI, ExPASy, EBI, Israel, Japan]
Baumann U., Huber R., Bode W., Grosse D., Lesjak M., Laurell C.-B.;
"Crystal structure of cleaved human alpha 1-antichymotrypsin at 2.7-A resolution and its comparison with other serpins.";
J. Mol. Biol. 218:595-606(1991).
- [9] X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS).
MEDLINE=96433079; PubMed=8836107; [NCBI, ExPASy, EBI, Israel, Japan]
Lukacs C.M., Zhong J.Q., Plotnick M.J., Rubin H., Cooperman B.S., Christianson D.W.;
"Arginine substitutions in the hinge region of antichymotrypsin affect serpin beta-sheet rearrangement.";
Nat. Struct. Biol. 3:888-893(1996).
- [10] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE=98198038; PubMed=9521649; [NCBI, ExPASy, EBI, Israel, Japan]
Lukacs C.M., Rubin H., Christianson D.W.;
"Engineering an anion-binding cavity in antichymotrypsin modulates the 'spring-loaded' serpin-protease interaction.";
Biochemistry 37:3297-3304(1998).
- [11] VARIANT ISEHARA-1.
MEDLINE=92316200; PubMed=1618300; [NCBI, ExPASy, EBI, Israel, Japan]
Tsuda M., Sei Y., Yamamura M., Yamamoto M., Shinohara Y.;
"Detection of a new mutant alpha-1-antichymotrypsin in patients with occlusive-cerebrovascular disease.";
FEBS Lett. 304:66-68(1992).
- [12] VARIANT BONN-1.
MEDLINE=92292844; PubMed=1351206; [NCBI, ExPASy, EBI, Israel, Japan]
Poller W., Faber J.-P., Scholz S., Weindinger S., Bartholome K., Olek K., Eriksson S.;
"Mis-sense mutation of alpha 1-antichymotrypsin gene associated with chronic lung disease.";
Lancet 339:1538-1538(1992).

Comments

- **FUNCTION:** ALTHOUGH ITS PHYSIOLOGICAL FUNCTION IS UNCLEAR, IT CAN INHIBIT NEUTROPHIL CATHEPSIN G AND MAST CELL CHYMASE, BOTH OF WHICH CAN CONVERT ANGIOTENSIN I TO THE ACTIVE ANGIOTENSIN II.
- **SUBCELLULAR LOCATION:** Extracellular.
- **TISSUE SPECIFICITY:** PLASMA. SYNTHESIZED IN THE LIVER. LIKE THE RELATED ALPHA-1-ANTITRYPSIN, ITS CONCENTRATION INCREASES IN THE ACUTE PHASE OF INFLAMMATION OR INFECTION.
- **DISEASE:** DEFICIENCY IN ACT CAN BE A CAUSE OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE (COPD) OR OF OCCLUSIVE CEREBROVASCULAR DISEASE.
- **MISCELLANEOUS:** ALPHA-1-ANTICHYMOTRYPSIN CAN BIND DNA.
- **SIMILARITY:** BELONGS TO THE SERPIN FAMILY.
- **CAUTION:** IT IS UNCERTAIN WHETHER MET-1 OR MET-4 IS THE INITIATOR.

Copyright

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

Cross-references

EMBL	K01500; AAA51543.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	X68733; CAA48671.1; ALT_INIT. [EMBL / GenBank / DDBJ] [CoDingSequence]
	X68734; CAA48671.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	X68735; CAA48671.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	X68736; CAA48671.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	X68737; CAA48671.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	BC003559; AAH03559.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	BC010530; AAH10530.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	J05176; AAA51560.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	A01246; ITHUC.
	A34934; A34934.
PDB	S14806; S14806.
	2ACH; 15-JUL-93. [ExPASy / RCSB]
	3CAA; 25-FEB-98. [ExPASy / RCSB]
	4CAA; 25-FEB-98. [ExPASy / RCSB]
	1AS4; 25-FEB-98. [ExPASy / RCSB]
	Detailed list of linked structures.
GlycoSuiteDB	P01011 ; -.
SWISS-2DPAGE	P01011 ; HUMAN.
Siena-2DPAGE	P01011 ; -.
Genew	HGNC:16 ; SERPINA3.
MIM	107280 [NCBI / EBI].
GeneCards	SERPINA3 .
GeneLynx	SERPINA3 ; Homo sapiens.
SOURCE	SERPINA3 ; Homo sapiens.
Ensembl	P01011 ; Homo sapiens. [Entry / Contig view]
InterPro	IPR000215 ; Serpin.
	Graphical view of domain structure.
Pfam	PF00079 ; serpin; 2.
SMART	SM00093 ; SERPIN; 1.
PROSITE	PS00284 ; SERPIN; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain] .
BLOCKS	P01011 .
ProtoNet	P01011 .
ProtoMap	P01011 .
PRESAGE	P01011 .
DIP	P01011 .
ModBase	P01011 .

Keywords

Serpin; Serine protease inhibitor; Plasma; Acute phase; Glycoprotein; Signal; 3D-structure; Polymorphism; Disease mutation.

Features

Key	From	To	Length	Description
SIGNAL	1	23	23	
CHAIN	24	423	400	ALPHA-1-ANTICHYMOTRYPSIN.
ACT_SITE	383	384		REACTIVE BOND.
CARBOHYD	93	93		N-LINKED (GLCNAC...).
CARBOHYD	127	127		N-LINKED (GLCNAC...).
DNA_BIND	235	237	3	
VARIANT	9	9		A -> T (IN DBSNP:4934) [NCBI/Ensembl]. /FTId=VAR_006973.

VARIANT	78	78	
VARIANT	167	167	
VARIANT	252	252	
VARIANT	401	401	
VARIANT	407	407	
CONFLICT	69	69	
CONFLICT	102	116	
CONFLICT	123	128	
CONFLICT	199	199	
CONFLICT	361	363	
CONFLICT	421	423	
HELIX	49	67	19
TURN	69	70	2
STRAND	73	75	3
HELIX	77	88	12
TURN	89	90	2
HELIX	93	102	10
TURN	103	104	2
TURN	107	109	3
HELIX	112	126	15
STRAND	128	129	2
STRAND	134	144	11
TURN	145	146	2
HELIX	151	161	11
STRAND	164	168	5
TURN	170	171	2
HELIX	173	187	15
TURN	188	190	3
TURN	201	202	2
STRAND	203	217	15
HELIX	223	225	3
STRAND	227	234	8
TURN	235	236	2
STRAND	237	256	20
TURN	257	260	4
STRAND	261	268	8
STRAND	272	279	8
TURN	281	282	2
HELIX	284	289	6
TURN	290	290	1
HELIX	293	302	10
STRAND	304	314	11
STRAND	316	323	8
HELIX	325	330	6
TURN	331	332	2
HELIX	335	337	3
TURN	339	340	2
HELIX	344	347	4
STRAND	352	365	14

L -> P (IN COPD; BOCHUM-1;
 DBSNP:1800463) [NCBI/Ensembl].
 /FTid=VAR_006974.
 A -> G.
 /FTid=VAR_006975.
 P -> A (IN COPD; BONN-1).
 /FTid=VAR_006976.
 M -> V (IN COPD; ISEHARA-1).
 /FTid=VAR_006977.
 D -> G (IN DBSNP:10956)
 [NCBI/Ensembl].
 /FTid=VAR_011742.
 P -> L (IN REF. 1).
 GLKFNLTTETSEAEIH -> ASSSPHGDLLRQKFT
 (IN REF. 1).
 LRTLNQ -> RAPSIS (IN REF. 1).
 L -> P (IN REF. 1).
 AVL -> VVS (IN REF. 1).
 KQA -> SKPRACIKQWGSQ (IN REF. 1).



Feature
aligner



Feature
table
viewer

STRAND	369	382	14
STRAND	391	394	4
STRAND	399	405	7
TURN	406	407	2
STRAND	413	417	5
TURN	420	421	2

Sequence information

Length: 423 AA [This is the length of the unprocessed precursor] Molecular weight: 47650 Da [This is the MW of the unprocessed precursor] CRC64: B002F946C86A8951 [This is a checksum on the sequence]

10	20	30	40	50	60
MERMLPLLAL	GLLAAGFCPA	VLCHPNPLD	EENLTQENQD	RGTHVDLGLA	SANVDFAFSL
70	80	90	100	110	120
YKQLVLKAPD	KNVIFSPLSI	STALAFSLG	AHNTTLTEIL	KGLKFNLTTT	SEAEIHQSFG
130	140	150	160	170	180
HLLRTLQSS	DELQLSMGNA	MFVKEQLSLL	DRFTEDAKRL	YGSEAFATDF	QDSAAAKLI
190	200	210	220	230	240
NDYVKNTRG	KITDLIKDLD	SQTMVLVNY	IFFKAKWEMP	FDPQDTHQSR	FYLSKKKWVM
250	260	270	280	290	300
VPMSLHHLT	IPYFRDEELS	CTVVELKYTG	NASALFILPD	QDKMEEVEAM	LLPETLKRWR
310	320	330	340	350	360
DSLEFREIGE	LYLPKFSISR	DYNLNDILLQ	LGIEEAFTSK	ADLSGITGAR	NLAVSQVVK
370	380	390	400	410	420
AVLDVFEEGT	EASAATAVKI	TLLSALVETR	TIVRFNRPF	MIIVPTDTQN	IFFMSKVTNP

KQA

P01011 in FASTA format

[View entry in original SWISS-PROT format](#)[View entry in raw text format \(no links\)](#)[Report form for errors/updates in this SWISS-PROT entry](#)Direct BLAST submission at
EMBnet-CH/SIB (Switzerland)

Direct BLAST submission at NCBI (Bethesda, USA)



ScanProsite, MotifScan

Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#), [Dotlet](#) (Java)

Feature table viewer (Java)



Search the SWISS-MODEL Repository

[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[SWISS-PROT](#)